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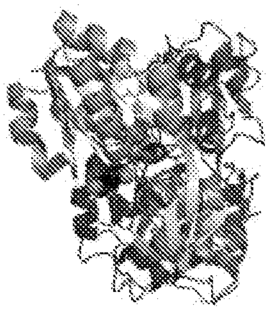
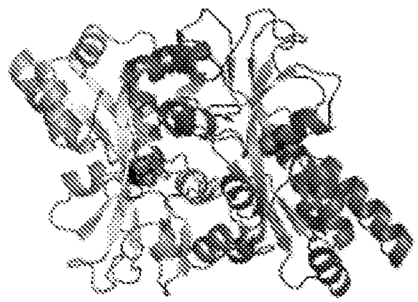
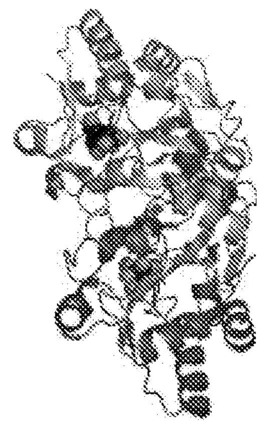
Periplasmic binding protein



Main view



Bottom view



Right view

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  - A B 229 a.a.
- Ligands
  - FLC ×2
- Waters ×349

Tools

- Image Generation
- AstexViewer™@MSD-EBI
- Run PROCHECK
- Clefts Calculation

PDB id:	2hxw
Name:	Periplasmic binding protein
Title:	Crystal structure of peb3 from campylobacter jejuni
Structure:	Major antigenic peptide peb3. Chain: a, b. Engineered: ye
Source:	Campylobacter jejuni. Strain: nctc 11168. Gene: peb3. Ex escherichia coli.
UniProt:	Chains A, B: Q0PBL7 (Q0PBL7_CAMJE) [Pfam

Seq: 250

Struc: 229

Key: PfamA domain Secondary structur

Resolution:	1.60Å
R-factor:	0.188
R-free:	0.212
Authors:	E.S.Rangarajan,S.Bhatia,D.C.Watson,C.Munger,M.Cygler A.Matte,N.M.Young,Montreal-Kingston Bacterial Structura Initiative (Bsgi)
Key ref:	E.S.Rangarajan et al. (2007). Structural context for protei glycosylation in bacteria: The structure of PEB3, an adhes Campylobacter jejuni.. *Protein Sci*, 16, 990-995. [PubMed id: 17456748] [DOI: 10.1110/ps.062737507]
Date:	04-Aug-06
Release date:	01-May-07

DOI no: 10.1110/ps.062737507
PubMed id: 17456748

Key
Protein Sci 16:99

Structural context for protein N-glycosylation in bacteria: The structure of PEB3, an adhesin from Cam jejuni.

E.S.Rangarajan, S.Bhatia, D.C.Watson, C.Munger, M.Cygler, A.Matte, N.M.Young.

ABSTRACT

Campylobacter jejuni is unusual among bacteria in possessing a eukaryotic-like system for N-linked protein glycosylatio residues in sequons of the type Asp/Glu-Xaa-Asn-Xaa-Ser/Thr. However, little is known about the structural context glycosylated sequons, limiting the design of novel recombinant glycoproteins. To obtain more information on sequon st we have determined the crystal structure of the PEB3 (Cj0289c) dimer. PEB3 has the class II periplasmic-binding prote with each monomer having two domains with a ligand-binding site containing citrate located between them, and ov resembles molybdate- and sulfate-binding proteins. The sequon around Asn90 is located within a surface-exposed loop two structural elements. The three key residues are well exposed on the surface; hence, they may be accessible to th oligosaccharyltransferase in the folded state.

Selected figure(s)

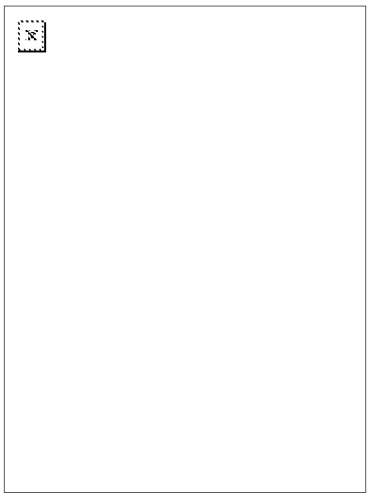

Figure 2.
Figure 2. PEB3-binding site and sequon structure. (A) Citrate binding-site density, 2F0-FC (omit) electron density map contour

Literature references that cite this PDB file's key reference

PubMed id Reference
18316380 T.D.Ho, B.M.Davis, J.M.Ritchie, and M.K.Waldor (2008).
Type 2 secretion promotes enterohemorrhagic Escherichia coli adherence and intestinal colonization.
Infect Immun, 76, 1858-1865.

The most recent references are shown first. Citation data come partly from CiteXplore and partly from an automated ha Note that this is likely to be only a partial list as not all journals are covered by either method. However, we are continua citation data so more and more references will be included with time.